

RAW SEQUENCE LISTING

EFS

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/817,483A
Source: 1FW16
Date Processed by STIC: 2/12/07

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 02/12/2007

PATENT APPLICATION: US/10/817,483A

TIME: 14:20:33

Input Set : N:\efs\02_12_07\10817483a_efs\0803R_AMDSEQLIST.TXT

Output Set: N:\CRF4\02122007\J817483A.raw

4 <110> APPLICANT: Habben, Jeffrey E.
 5 Zinselmeier, Christopher
 6 Tomes, Dwight
 7 Abbitt, Shane
 8 Helentjaris, Timothy G.
 9 Niu, Xiaomu
 13 <120> TITLE OF INVENTION: Modulation of Cytokinin Activity in
 14 Plants
 16 <130> FILE REFERENCE: 0803R
 18 <140> CURRENT APPLICATION NUMBER: US 10/817,483A
 19 <141> CURRENT FILING DATE: 2004-04-02
 21 <150> PRIOR APPLICATION NUMBER: US 60/460,718
 22 <151> PRIOR FILING DATE: 2003-04-04
 24 <150> PRIOR APPLICATION NUMBER: US 09/545,334
 25 <151> PRIOR FILING DATE: 2000-04-07
 27 <150> PRIOR APPLICATION NUMBER: US 60/129,844
 28 <151> PRIOR FILING DATE: 1999-04-16
 30 <160> NUMBER OF SEQ ID NOS: 43
 32 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 34 <210> SEQ ID NO: 1
 35 <211> LENGTH: 1919
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Agrobacterium tumefaciens
 39 <220> FEATURE:
 40 <221> NAME/KEY: CDS
 41 <222> LOCATION: (690)...(1411)
 42 <223> OTHER INFORMATION: ipt
 44 <400> SEQUENCE: 1
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 47 aagtttgcaa taatatgcta atgtaaaatt aaaaaattat gtactgccgc atttgttcaa 180
 48 atggcgccgt tatttcaaaa atatctttga tttgtgtacg aggacaacga ctgcaggaag 240
 49 taaataaaaag acgctgttgt taagaaattg ctatcatatg tgcccagcta tagggccatt 300
 50 taagtccaat tgtgaaatag ccgcccttat tttgacgtct catcaaatca aatattaaaa 360
 51 aatatctcac tctgtcgcca gcaatgatgt aataaccgca gaaaagtga agtaaatcgc 420
 52 ggaaaaacgt cgccgagtgg catgaatagc ggccctcgta ttgctgattt agtcagcttt 480
 53 atttgactta agggtgccct cgtttagtgac aaattgcttt caaggagaca gccatgcccc 540
 54 acactttgtt gaaaaacaag ttgccttttg ggaagaacct aaagccactt gctcttcaag 600
 55 gaggaatatc gaggaagaga atataacagc ctctgtgtaca gacttctctt gtgcaaaaaat 660
 56 caatttgtat tcaacatatc gcaagaccg atg gat cta cgt cta att ttc ggt 713
 57 Met Asp Leu Arg Leu Ile Phe Gly
 58 1 5
 60 cca act tgc aca gga aag aca tcg act gcg ata gct ctt gcc cag cag 761

see p. 6

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64 act ggc ctc cca gtc ctc tcg ctc gat cgc gtc caa tgc tgt cct caa      809
65 Thr Gly Leu Pro Val Leu Ser Leu Asp Arg Val Gln Cys Cys Pro Gln
66 25                      30                      35                      40
68 cta tca acc gga agc ggg cga cca aca gtg gaa gaa ctg aaa gga acg      857
69 Leu Ser Thr Gly Ser Gly Arg Pro Thr Val Glu Glu Leu Lys Gly Thr
70                      45                      50                      55
72 act cgt ctg tac ctt gat gat cgc cct ttg gta aag ggt atc att aca      905
73 Thr Arg Leu Tyr Leu Asp Asp Arg Pro Leu Val Lys Gly Ile Ile Thr
74                      60                      65                      70
76 gcc aag caa gct cat gaa cgg ctc att gcg gag gtg cac aat cac gag      953
77 Ala Lys Gln Ala His Glu Arg Leu Ile Ala Glu Val His Asn His Glu
78                      75                      80                      85
80 gcc aaa ggc ggg ctt att ctt gag gga gga tct atc tcg ttg ctc agg      1001
81 Ala Lys Gly Gly Leu Ile Leu Glu Gly Gly Ser Ile Ser Leu Leu Arg
82 90                      95                      100
84 tgc atg gcg caa agt cgt tat tgg aac gcg gat ttt cgt tgg cat att      1049
85 Cys Met Ala Gln Ser Arg Tyr Trp Asn Ala Asp Phe Arg Trp His Ile
86 105                      110                      115                      120
88 att cgc aac gag tta gca gac gag gag agc ttc atg agc gtg gcc aag      1097
89 Ile Arg Asn Glu Leu Ala Asp Glu Glu Ser Phe Met Ser Val Ala Lys
90                      125                      130                      135
92 acc aga gtt aag cag atg tta cgc ccc tct gca ggt ctt tct att atc      1145
93 Thr Arg Val Lys Gln Met Leu Arg Pro Ser Ala Gly Leu Ser Ile Ile
94                      140                      145                      150
96 caa gag ttg gtt caa ctt tgg agg gag cct cgg ctg agg ccc ata ctg      1193
97 Gln Glu Leu Val Gln Leu Trp Arg Glu Pro Arg Leu Arg Pro Ile Leu
98                      155                      160                      165
100 gaa ggg atc gat gga tat cga tat gcc ctg cta ttt gct acc cag aac      1241
101 Glu Gly Ile Asp Gly Tyr Arg Tyr Ala Leu Leu Phe Ala Thr Gln Asn
102 170                      175                      180
104 cag atc acg ccc gat atg cta ttg cag ctc gac gca gat atg gag aat      1289
105 Gln Ile Thr Pro Asp Met Leu Leu Gln Leu Asp Ala Asp Met Glu Asn
106 185                      190                      195                      200
108 aaa ttg att cac ggt atc gct cag gag ttt cta atc cat gcg cgt cga      1337
109 Lys Leu Ile His Gly Ile Ala Gln Glu Phe Leu Ile His Ala Arg Arg
110                      205                      210                      215
112 cag gaa cag aaa ttc cct ttg gtg ggc gcg aca gct gtc gaa gcg ttt      1385
113 Gln Glu Gln Lys Phe Pro Leu Val Gly Ala Thr Ala Val Glu Ala Phe
114                      220                      225                      230
116 gaa gga cca cca ttt cga atg tga ta gattgcacca gttttgtttc      1431
117 Glu Gly Pro Pro Phe Arg Met *
118                      235
120 agacttgctg ctatttgaat aagatgttcg ttctttgttg tgttggtgtg ttgtgataga 1491
121 ggcaagtggg ttgaaacttg tttttactgg tttattttca gtctcttgga cgatgtttta 1551
122 caaatataat attgtgaaaa ttgtggtttt atattcgtag aacgaaataa atggtaagta 1611
123 tagccgttat caaaaatttag caaaaattgt taaaggttct tttatgcggt gaggtgtcgc 1671
124 acttttcatc attgtcgcgt aaggagttac ggatatccat aactgtaaaa acgccgcaga 1731

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125 atttacgggt ggtgcattta gtttgccgtt caacatgatt ttggcaatag ttggtaacca 1791
 126 agcactagcc aaccgttcga taatcactta atcgatggaa ccgttcagct ttccttcgtg 1851
 127 aggctgctct tgatgatgag ctgccgtcta gtttttataa cgccgggtta cgcattatag 1911
 128 acaagctt 1919

130 <210> SEQ ID NO: 2

131 <211> LENGTH: 239

132 <212> TYPE: PRT

133 <213> ORGANISM: Agrobacterium tumefaciens

135 <400> SEQUENCE: 2

136 Met Asp Leu Arg Leu Ile Phe Gly Pro Thr Cys Thr Gly Lys Thr Ser
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 138 Thr Ala Ile Ala Leu Ala Gln Gln Thr Gly Leu Pro Val Leu Ser Leu
 139 20 25 30
 140 Asp Arg Val Gln Cys Cys Pro Gln Leu Ser Thr Gly Ser Gly Arg Pro
 141 35 40 45
 142 Thr Val Glu Glu Leu Lys Gly Thr Thr Arg Leu Tyr Leu Asp Asp Arg
 143 50 55 60
 144 Pro Leu Val Lys Gly Ile Ile Thr Ala Lys Gln Ala His Glu Arg Leu
 145 65 70 75 80
 146 Ile Ala Glu Val His Asn His Glu Ala Lys Gly Gly Leu Ile Leu Glu
 147 85 90 95
 148 Gly Gly Ser Ile Ser Leu Leu Arg Cys Met Ala Gln Ser Arg Tyr Trp
 149 100 105 110
 150 Asn Ala Asp Phe Arg Trp His Ile Ile Arg Asn Glu Leu Ala Asp Glu
 151 115 120 125
 152 Glu Ser Phe Met Ser Val Ala Lys Thr Arg Val Lys Gln Met Leu Arg
 153 130 135 140
 154 Pro Ser Ala Gly Leu Ser Ile Ile Gln Glu Leu Val Gln Leu Trp Arg
 155 145 150 155 160
 156 Glu Pro Arg Leu Arg Pro Ile Leu Glu Gly Ile Asp Gly Tyr Arg Tyr
 157 165 170 175
 158 Ala Leu Leu Phe Ala Thr Gln Asn Gln Ile Thr Pro Asp Met Leu Leu
 159 180 185 190
 160 Gln Leu Asp Ala Asp Met Glu Asn Lys Leu Ile His Gly Ile Ala Gln
 161 195 200 205
 162 Glu Phe Leu Ile His Ala Arg Arg Gln Glu Gln Lys Phe Pro Leu Val
 163 210 215 220
 164 Gly Ala Thr Ala Val Glu Ala Phe Glu Gly Pro Pro Phe Arg Met
 165 225 230 235

168 <210> SEQ ID NO: 3

169 <211> LENGTH: 2085

170 <212> TYPE: DNA

171 <213> ORGANISM: Zea mays

173 <220> FEATURE:

174 <221> NAME/KEY: promoter

175 <222> LOCATION: (1)...(2085)

176 <223> OTHER INFORMATION: zag2.1

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179 agcttcgtgt gttccttcga tcggtcacag ttgattcct gctcaccaca tatttttgcc 60

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182 tgtctctaatt ttagcagcag gtcttgagtt tgattcacaa ttcttgcaga tttatttttt 240
183 gagccataac agggatgagg gcaaaatagg aaatgaacga catgttacct ttaccgcctt 300
184 aataagtagt agagatatcc agtttatacg taattattat tatataaaat gcactgcaca 360
185 tataattacta ttaccagttt tcttggacat gcacagcaga aaacacgcac acgcagagag 420
186 gaaaaggaga ggccataaac caaaaggcct taagaatata tgtaaagata tgtctaaatg 480
187 gctatatctg gttaagcaag ataacagggc tctggtcatc agtagtagtg gccttttgcc 540
188 cttgcccctc atctctctca cacctctctt ttctcagcct tgcttccgat cgatggatcc 600
189 catcccactg ccatagtgcc atcctttctt tcccttgccg gcattgccta gccggccggc 660
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211 cgtagtgtac tgtactactg cggctagcta gatcttccaa gctagctata gttcgccggt 1980
212 ccccttgatc tgcttcacag aacatatata acacttgaac tcttttacgc ttatgagaaa 2040
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215 <210> SEQ ID NO: 4

216 <211> LENGTH: 344

217 <212> TYPE: DNA

218 <213> ORGANISM: Cauliflower mosaic virus

220 <220> FEATURE:

221 <221> NAME/KEY: enhancer

222 <222> LOCATION: (1)...(344)

223 <223> OTHER INFORMATION: CaMV35s

225 <400> SEQUENCE: 4

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228 acctcctcgg attccattgc ccagctatct gtcacttcat caaaaggaca gtagaaaagg 180
229 aaggtggcac ctacaaatgc catcattgct ataaaggaaa ggctatcgtt caagatgcct 240
230 ctgccgacag tgggtcccaa gatggacccc caccacgag gagcatcgtg gaaaaagaag 300
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235 <212> TYPE: DNA
236 <213> ORGANISM: Zea mays
238 <220> FEATURE:
239 <221> NAME/KEY: promoter
240 <222> LOCATION: (1)...(2198)
241 <223> OTHER INFORMATION: ZmMADS
243 <400> SEQUENCE: 5
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246 ttacatgtcc ttcttctgct gttgctgctt gagcaggata tagagagatg accgacaccg 180
247 ggttgatctt gggacaacct tcttctcatc ttttcttcgt tgttttcttt tctattctca 240
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249 catacagagg aggaacccga agactatgaa ccatgtacaa cagtcttcaa cccaagaatc 360
250 accaagcatt gtgatcttag gggcgaggga gtggaaaaatg gagttgcttg tgatttggca 420
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255 ggggcacaag tgagtgggtg ggtcgatgac cctgatgttt gtggtctctg gttccaagaa 720
256 tctttgtctc tctttatgat aataacttct tttgtcgtcc ttttctgttt actttgactc 780
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277 cactcgaacg ccggcctcgc taggcccata cttctggccc gcaataacga tccccgtcat 2040
278 gatccgacgg tctagctgcc tccacgccgc tccaaaaccc ccgcgtccaa tcaaaacacg 2100
279 acagcgggac gagcgaaacc accgtggttt cgccaaacgg ctttcttcc catctaaaaa 2160
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282 <210> SEQ ID NO: 6
283 <211> LENGTH: 1470
284 <212> TYPE: DNA

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:35; N Pos. 1366,1626,1629

VERIFICATION SUMMARY

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L:1677 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35

L:1700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:1320

M:341 Repeated in SeqNo=35